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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GCACGAGAGTCAGCATGGGGGCCTGGACCAAGACGGGGAGGCCCGGCCTGCCCTTGACGG 1920

Qy        639 ySerAlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetPr 659
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TAGCGCCGCCCTGCAACCCCTGCTGCACACGGTGAAAGCCGGCAGCCCCTCGGACATGCC 1980

Qy        659 oArgAspSerGlyIleTyrAspSerSerValProSerSerGluLeuSerLeuProLeuMe 679
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTCTCTGCCACTGAT 2040

Qy        679 tGluGlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSe 699
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GGAAGGACTCTCGACGGACCAGACAGAAACGTCTTCCCTGACGGAGAGCGTGTCCTCCTC 2100

Qy        699 rSerGlyLeuGlyGluGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySe 719
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TTCAGGCCTGGGTGAGGAGGAACCTCCTGCCCTTCCTTCCAAGCTCCTCTCTTCTGGGTC 2160

Qy        719 rCysLysAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ATGCAAAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCCT 2218
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RESULT 14
US-09-863-818A-9
; Sequence 9, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)..(2283)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (118)..()
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (170)..(170)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (194)..(194)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
US-09-863-818A-9

Alignment Scores:
Pred. No.: 0 Length: 2786

Score:	3835.50	Matches:	722
Percent Similarity:	98.2%	Conservative:	3
Best Local Similarity:	97.8%	Mismatches:	12
Query Match:	97.2%	Indels:	1
DB:	3	Gaps:	1

US-10-616-788-2 (1-738) x US-09-863-818A-9 (1-2786)

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Qy          1 MetAlaProTrpLeuGlnLeuCysSerValPhePheThrValAsnAlaCysLeuAsnGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 ATGGCCCCGTGGCTGCAGCTCTGCTCCGTCTTCTTTACGGTCAACGCCTGCCTCAACGGC 129

Qy         21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTrpGlyValAspThrCysGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 TCGCAGCTGGCTGTNGCCGCTGGCGGGTCCGGCCGCGCGCNGGGCGCCGACACCTGTAGC 189

Qy         41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLysTyr 60
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGGANGGGAGTGGGGCCAGCCAGCAGAAACAGTGGGCTGTACAACATCACCTTCAAATAT 249

Qy         61 AspAsnCysThrThrTyrLeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACAATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAAT 309

Qy         81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 ATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTCTTTGGTCCCCA 369

Qy        101 GlyAlaLeuGlyIleGluPheLeuLysGlyPheArgValIleLeuGluGluLeuLysSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCG 429

Qy        121 GluGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
              ||||||||||||  ||||||||||||||||||||||||||||||  ||||||||||||
Db        430 GAGGGAAGACAGNGCCAACAACTGATTCTAAAGGATCCGAAGCAGNTCAACAGTAGCTTC 489

Qy        141 LysArgThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPhe 160
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        490 AAAAGAACTGGAATGGAATCTCAACCTTTNCTGAATATGAAATTTGAAACGGATTATTTC 549

Qy        161 ValLysValValProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhePhe 180
              |||:::  :::  |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GTAAGG---TTGTCCTTTTCCTTCATTAAAAACGAAAGCAATTACCACCCTTTCTTCTTT 606

Qy        181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AGAACCCGAGCCTGTGACCTGTTGTTACAGCCGGACAATCTAGCTTGTAAACCCTTCTGG 666

Qy        201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGCAGGTGTCCTTCGACCAC 726

Qy        221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLeuLysHisGluGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GCACCGCACAACTTCGGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGGA 786

Qy        241 ProPheLysArgLysThrCysLysGlnGluGlnThrThrGluThrThrSerCysLeuLeu 260
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        787 CCTTTCAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGATGACCAGCTGCCTCCTT 846

Qy        261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrThrArg 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 CAAAATGTTTCTCCAGGGGATTATATAATTGAGCTGGTGGATGACACTAACACAACAAGA 906

Qy        281 LysValMetHisTyrAlaLeuLysProValHisSerProTrpAlaGlyProIleArgAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGGCCCATCAGAGCC 966

Qy        301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATG 1026

Qy        321 CysArgLysLysGlnGlnGluAsnIleTyrSerHisLeuAspGluGluSerSerGluSer 340
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Db       1027 TGCCGCAAGAAGCAACAAGAAAATATATATTCACATTTAGATGAAGAGAGCTCTGAGTCT 1086

Qy        341 SerThrTyrThrAlaAlaLeuProArgGluArgLeuArgProArgProLysValPheLeu 360

Db       1087 TCCACATACACTGCAGCACTCCCAAGAGAGAGGCTCCGGCCGCGGCCGAAGGTCTTTCTC 1146

Qy        361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380

Db       1147 TGCTATTCCAGTAAAGATGGCCAGAATCACATGAATGTCGTCCAGTGTTTCGCCTACTTC 1206

Qy        381 LeuGlnAspPheCysGlyCysGluValAlaLeuAspLeuTrpGluAspPheSerLeuCys 400

Db       1207 CTCCAGGACTTCTGTGGCTGTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGT 1266

Qy        401 ArgGluGlyGlnArgGluTrpValIleGlnLysIleHisGluSerGlnPheIleIleVal 420

Db       1267 AGAGAAGGGCAGAGAGAATGGGTCATCCAGAAGATCCACGAGTCCCAGTTCATCATTGTG 1326

Qy        421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisLysGlyGly 440

Db       1327 GTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAAGGAGGT 1386

Qy        441 GlyArgGlySerGlyLysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLys 460

Db       1387 GGCCGAGGCTCGGGGAAAGGAGAGCTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAG 1446

Qy        461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480

Db       1447 CTCCGCCAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTT 1506

Qy        481 AspTyrSerCysGluGlyAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeu 500

Db       1507 GATTATTCCTGCGAGGGAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTC 1566

Qy        501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520

Db       1567 ATGGACAATCTTCCTCAGCTCTGTTCCCACCTGCACTCCCGAGACCACGGCCTCCAGGAG 1626

Qy        521 ProGlyGlnHisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArg 540

Db       1627 CCGGGGCAGCACACGCGACAGGGCAGCAGAAGGAACTACTTCCGGAGCAAGTCAGGCCGG 1686

Qy        541 SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGluGluProAspTrpPhe 560

Db       1687 TCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGCCCGACTGGTTC 1746

Qy        561 GluLysGlnPheValProPheHisProProProLeuArgTyrArgGluProValLeuGlu 580

Db       1747 GAAAAGCAGTTCGTTCCCTTCCATCCTCCTCCACTGCGCTACCGGGAGCCAGTCTTGGAG 1806

Qy        581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGluSerAsp 600

Db       1807 AAATTTGATTCGGGCTTGGTTTTAAATGATGTCATGTGCAAACCAGGGCCTGAGAGTGAC 1866

Qy        601 PheCysLeuLysValGluAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHis 620

Db       1867 TTCTGCCTAAAGGTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCCAGCAC 1926

Qy        621 GluSerGlnHisGlyGlyLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySer 640

Db       1927 GAGAGTCAGCATGGGGGCCTGGACCAAGACGGGGAGGCCCGGCCTGCCCTTGACGGTAGC 1986

Qy        641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArg 660

Db       1987 GCCGCCCTGCAACCCCTGCTGCACACGGTGAAAGCCGGCAGCCCCTCGGACATGCCGCGG 2046

Qy        661 AspSerGlyIleTyrAspSerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680

Db       2047 GACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTCTCTGCCACTGATGGAA 2106

Qy        681 GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSerSer 700
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Db       2107 GGACTCTCGACGGACCAGACAGAAACGTCTTCCCTGACGGAGAGCGTGTCCTCCTCTTCA 2166

Qy        701 GlyLeuGlyGluGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720

Db       2167 GGCCTGGGTGAGGAGGAACCTCCTGCCCTTCCTTCCAAGCTCCTCTCTTCTGGGTCATGC 2226

Qy        721 LysAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738

Db       2227 AAAGCAGATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCCT 2280
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RESULT 15
US-10-749-144-9
; Sequence 9, Application US/10749144
; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)..(2283)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (118)..()
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (170)..(170)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (194)..(194)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
US-10-749-144-9

Alignment Scores:

Pred. No.:	0	Length:	2786
Score:	3835.50	Matches:	722
Percent Similarity:	98.2%	Conservative:	3
Best Local Similarity:	97.8%	Mismatches:	12
Query Match:	97.2%	Indels:	1
DB:	8	Gaps:	1

US-10-616-788-2 (1-738) x US-10-749-144-9 (1-2786)

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Qy        587 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 646
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660

Qy        647 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 720

Qy        707 PPALPSKLLSSGSCKADLGCRSYTDELHAVAP 738
              |||||||||||||||||||||||||| ||
Db        721 PPALPSKLLSSGSCKADLGCRSYTDELHAAAP 752
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RESULT 13
US-09-863-818A-10
; Sequence 10, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
; NAME/KEY: misc_feature
; LOCATION: (26)..(26)
; OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc_feature
; LOCATION: (109)..(109)
; OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc_feature
; LOCATION: (120)..(120)
; OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc_feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (170)..(170)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (194)..(194)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
US-09-863-818A-10

Query Match 97.2%; Score 3835.5; DB 3; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;

Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

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Qy          1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRAWGVDTCGWRGVGPASRNSGLYNITFKY 60
              |||||||||||||||||||||||||||||||| | ||| | ||||||||||||||||||
Db          1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRAXGADTCSWXGVGPASRNSGLYNITFKY 60

Qy         61 DNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKS 120

Qy        121 EGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFF 180
              |||| |||||||||| |||||||||||||| ||||||||||: : | ||||||||||||
Db        121 EGRQXQQLILKDPKQXNSSFKRTGMESQPXLNMKFETDYFVR-LSFSFIKNESNYHPFFF 179

Qy        181 RTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 RTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEG 239

Qy        241 PFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRA 300
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        240 PFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRA 299

Qy        301 MAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFL 360
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 VAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFL 359

Qy        361 CYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIV 419

Qy        421 VCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYF 480
              -||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 VCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYF 479

Qy        481 DYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGR 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 DYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGR 539

Qy        541 SLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESD 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 SLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESD 599

Qy        601 FCLKVEAPVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPR 660
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 FCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPR 659

Qy        661 DSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 DSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSC 719

Qy        721 KADLGCRSYTDELHAVAP 738
              ||||||||||||||||||
Db        720 KADLGCRSYTDELHAVAP 737
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RESULT 14
US-10-749-144-10
; Sequence 10, Application US/10749144
; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens